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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=4; day=15; hr=18; min=35; sec=53; ms=492;]

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Application No: 10564665 Version No: 2.0

Input Set:

Output Set:

Started: 2008-04-01 10:59:55.302
Finished: 2008-04-01 10:59:57.381
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 79 ms
Total Warnings: 21
Total Errors: 0
No. of SeqIDs Defined: 31
Actual SeqID Count: 31

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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Error code Error Description

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SEQUENCE LISTING

<110> Irie, Reiko
Tsunoda, Hiroyuki
Igawa, Tomoyuki
Sekimori, Yasuo
Tsuchiya, Masayuki

<120> IgM PRODUCTION BY TRANSFORMED CELL AND
METHOD OF QUANTIFYING THE SAME

<130> 14875-155US1

<140> 10564665
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<151> 2004-07-15

<150> US 60/487,333
<151> 2003-07-15

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<170> PatentIn version 3.1

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cct ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

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Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala
65 70 75 80

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acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	100	105	110	336
tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala	115	120	125	384
tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala	130	135	140	432
cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr	145	150	155	480
145	150	155	160	
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165	170	175		
atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr	180	185	190	576
180	185	190		
cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser	195	200	205	624
195	200	205		
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210	215	220		
gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg Val Val Cys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val	225	230	235	720
225	230	235	240	
cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val	245	250	255	768
245	250	255		
cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile	260	265	270	816
260	265	270		
tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu	275	280	285	864
275	280	285		
cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln	290	295	300	912
290	295	300		
gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca				960

Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr			
305	310	315	320
ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc			1008
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys			
325	330	335	
cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg			1056
Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met			
340	345	350	
tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca			1104
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro			
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Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu			
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Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg			
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Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His			
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ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat			1296
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp			
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Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp			
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ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc			1392
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala			
450	455	460	
ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg			1440
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu			
465	470	475	480
aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct			1488
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser			
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ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc			1536
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser			
500	505	510	
ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca			1584
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro			
515	520	525	
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Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp			

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Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
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aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc			1728
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
565	570	575	
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Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
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Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Lys Asn			
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Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr			
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Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser			
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Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr			
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Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
225 230 235 240

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Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
260 265 270

Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
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Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
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Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
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Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
325 330 335

Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
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370 375 380

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Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
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Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
465 470 475 480

Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
485 490 495

Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
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Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
515 520 525

Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
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Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
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Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30 96

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Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45 144

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Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
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Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
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Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95 288

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Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110 336

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